

0400

GW

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/021,811

DATE: 01/15/2002

TIME: 18:07:38

Input Set : A:\BB1294 USDIV Seq.txt

Output Set: N:\CRF3\01152002\J021811.raw

PS

3 <110> APPLICANT: Cahoon, Rebecca E.
 4 Fang, Yiwen
 5 Odell, Joan
 6 Weng, Zude
 8 <120> TITLE OF INVENTION: Plant Myb Transcription Factor Homologs
 10 <130> FILE REFERENCE: BB1294 US NA
 12 <140> CURRENT APPLICATION NUMBER: US/10/021,811
 13 <141> CURRENT FILING DATE: 2001-12-14
 15 <150> PRIOR APPLICATION NUMBER: 60/110,609
 16 <151> PRIOR FILING DATE: 1998-December-02
 18 <160> NUMBER OF SEQ ID NOS: 63
 20 <170> SOFTWARE: Microsoft Office 97
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 771
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Zea mays
 27 <220> FEATURE:
 28 <221> NAME/KEY: unsure
 29 <222> LOCATION: (4)
 31 <220> FEATURE:
 32 <221> NAME/KEY: unsure
 33 <222> LOCATION: (99)
 35 <220> FEATURE:
 36 <221> NAME/KEY: unsure
 37 <222> LOCATION: (396)
 39 <220> FEATURE:
 40 <221> NAME/KEY: unsure
 41 <222> LOCATION: (470)
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 44 <221> NAME/KEY: unsure
 45 <222> LOCATION: (486)
 47 <220> FEATURE:
 48 <221> NAME/KEY: unsure
 49 <222> LOCATION: (586)
 51 <220> FEATURE:
 52 <221> NAME/KEY: unsure
 53 <222> LOCATION: (600)
 55 <220> FEATURE:
 56 <221> NAME/KEY: unsure
 57 <222> LOCATION: (612)
 59 <220> FEATURE:
 60 <221> NAME/KEY: unsure
 61 <222> LOCATION: (615)
 63 <220> FEATURE:
 64 <221> NAME/KEY: unsure
 65 <222> LOCATION: (627)
 67 <220> FEATURE:

ENTERED

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68 <221> NAME/KEY: unsure
69 <222> LOCATION: (632)
71 <220> FEATURE:
72 <221> NAME/KEY: unsure
73 <222> LOCATION: (658)
75 <220> FEATURE:
76 <221> NAME/KEY: unsure
77 <222> LOCATION: (690)
79 <220> FEATURE:
80 <221> NAME/KEY: unsure
81 <222> LOCATION: (716)
83 <220> FEATURE:
84 <221> NAME/KEY: unsure
85 <222> LOCATION: (724)
87 <220> FEATURE:
88 <221> NAME/KEY: unsure
89 <222> LOCATION: (736)
91 <220> FEATURE:
92 <221> NAME/KEY: unsure
93 <222> LOCATION: (752)
95 <220> FEATURE:
96 <221> NAME/KEY: unsure
97 <222> LOCATION: (758)
99 <400> SEQUENCE: 1
W--> 100 caanccgctggg attgttcaat ccgttcgaca tcacaaaatc caccgcacaaa gaagcgacag 60
W--> 101 atgactacga gcaggggtggc caggtcgtgc ggccgcggna gcgacgatga gccggcggtg 120
102 cgcaaggggc cgtggacgct ggaggaggac ctcatcctcg tcagctacat ctcccagcac 180
103 ggggagggct cctgggacaa cctcgcgcg cgcagctggac tgaaccgcaa cggcaagagc 240
104 tgcaggctgc ggtggctcaa ctacctgagg ccgggggtgc ggcgcggcag catcacggcg 300
105 ggggaggaca cggctcatccg ggagctccac gcgaggtggg ggaacaagtg gtccaagatc 360
W--> 106 tccaagcacc tccccggccg aaccgcacaac gagatnaaga actactggag gaccaggatc 420
W--> 107 caacaagaag aacagcaagg agccaagacg acgcaacaac gggaccgtcn acgaccgcca 480
W--> 108 actccngggc ccggggacga ctactgggtg cacaaccgca ccccgacaac aagccatact 540
W--> 109 gcctgcaaaa accccatgca actgcacgcg acaacaaccg gtctcntaac aacaagacan 600
W--> 110 ccccttcggg gncctnacaac cagaaanccc cncggcgggg gaatggtaat cacaacanaa 660
W--> 111 attgtaccct ctgtccaact aaactttccn cggcacataa acgtcggctg accttnacaa 720
W--> 112 tcantcttct ccaactnatgc actttgcaac gngtgtantt tgataaacct t 771
114 <210> SEQ ID NO: 2
115 <211> LENGTH: 157
116 <212> TYPE: PRT
117 <213> ORGANISM: Zea mays
119 <220> FEATURE:
120 <221> NAME/KEY: UNSURE
121 <222> LOCATION: (111)
123 <220> FEATURE:
124 <221> NAME/KEY: UNSURE
125 <222> LOCATION: (136)
127 <400> SEQUENCE: 2
128 Thr Thr Ser Arg Val Ala Arg Ser Cys Gly Arg Gly Ser Asp Asp Glu

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```

129      1              5              10              15
131 Pro Ala Val Arg Lys Gly Pro Trp Thr Leu Glu Glu Asp Leu Ile Leu
132              20              25              30
134 Val Ser Tyr Ile Ser Gln His Gly Glu Gly Ser Trp Asp Asn Leu Ala
135              35              40              45
137 Arg Ala Ala Gly Leu Asn Arg Asn Gly Lys Ser Cys Arg Leu Arg Trp
138              50              55              60
140 Leu Asn Tyr Leu Arg Pro Gly Val Arg Arg Gly Ser Ile Thr Ala Gly
141 65              70              75              80
143 Glu Asp Thr Val Ile Arg Glu Leu His Ala Arg Trp Gly Asn Lys Trp
144              85              90              95
W--> 146 Ser Lys Ile Ser Lys His Leu Pro Gly Arg Thr Asp Asn Glu Xaa Lys
147              100              105              110
149 Asn Tyr Trp Arg Thr Arg Ile Gln Gln Glu Glu Gln Gln Gly Ala Lys
150              115              120              125
W--> 152 Thr Thr Gln Gln Arg Asp Arg Xaa Arg Pro Pro Thr Pro Gly Pro Gly
153              130              135              140
155 Asp Asp Tyr Trp Val His Asn Pro Thr Pro Thr Thr Ser
156 145              150              155
158 <210> SEQ ID NO: 3
159 <211> LENGTH: 782
160 <212> TYPE: DNA
161 <213> ORGANISM: Zea mays
163 <220> FEATURE:
164 <221> NAME/KEY: unsure
165 <222> LOCATION: (3)
167 <400> SEQUENCE: 3
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169 tactcttctc tgtactagct ttcttcttcc tctctcttcc ctcaaaaaca gactggattt 120
170 caacaagata atcctgaaac tggagccaac aagcacacag agaaagaaga gcaagaagac 180
171 cggctcccgag ccgatacaag gtaggagtga gcagcgttag ttcatcata tcgcataggc 240
172 gatatgggtga cagtgaagaga ggagactcgc aagggggccat ggacagagca ggaggacctg 300
173 caactgggtat gcactgtccg tctgttcggt gaacgtcgtt gggatttcat tgccaaagta 360
174 tcaggactca accggacagg caagagctgc cggctgcggt gggtcacta cctccaccct 420
175 ggcctcaage gtgggcgcat gtctcccat gaagagcgcc tcatccttga gctgcacgct 480
176 cgggtggggaa acaggtggtc caggatagca cggcgcttgc cagggcgcac tgacaatgag 540
177 atcaagaact actggaggac acacatgagg aagaaagcac aggagaggaa gaggaacatg 600
178 tctccatcat catctcatc ttactgagt taccagtcag gctaccaga tactccatca 660
179 atcattggag ttaagggaca ggagcttcat ggtggcagtg gctgcatcac aagcatcctg 720
180 aagggcaccc atccggacat ggatggctat cccatggacc agatatggat ggaattgaag 780
181 gg
183 <210> SEQ ID NO: 4
184 <211> LENGTH: 179
185 <212> TYPE: PRT
186 <213> ORGANISM: Zea mays
188 <400> SEQUENCE: 4
189 Met Val Thr Val Arg Glu Glu Thr Arg Lys Gly Pro Trp Thr Glu Gln
190 1 5 10 15
192 Glu Asp Leu Gln Leu Val Cys Thr Val Arg Leu Phe Gly Glu Arg Arg

```

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```

193          20          25          30
195 Trp Asp Phe Ile Ala Lys Val Ser Gly Leu Asn Arg Thr Gly Lys Ser
196          35          40          45
198 Cys Arg Leu Arg Trp Val Asn Tyr Leu His Pro Gly Leu Lys Arg Gly
199          50          55          60
201 Arg Met Ser Pro His Glu Glu Arg Leu Ile Leu Glu Leu His Ala Arg
202 65          70          75          80
204 Trp Gly Asn Arg Trp Ser Arg Ile Ala Arg Arg Leu Pro Gly Arg Thr
205          85          90          95
207 Asp Asn Glu Ile Lys Asn Tyr Trp Arg Thr His Met Arg Lys Lys Ala
208          100         105         110
210 Gln Glu Arg Lys Arg Asn Met Ser Pro Ser Ser Ser Ser Ser Ser Leu
211          115         120         125
213 Ser Tyr Gln Ser Gly Tyr Pro Asp Thr Pro Ser Ile Ile Gly Val Lys
214          130         135         140
216 Gly Gln Glu Leu His Gly Gly Ser Gly Cys Ile Thr Ser Ile Leu Lys
217 145          150          155          160
219 Gly Thr His Pro Asp Met Asp Gly Tyr Pro Met Asp Gln Ile Trp Met
220          165          170          175
222 Glu Leu Lys
225 <210> SEQ ID NO: 5
226 <211> LENGTH: 601
227 <212> TYPE: DNA
228 <213> ORGANISM: Zea mays
230 <220> FEATURE:
231 <221> NAME/KEY: unsure
232 <222> LOCATION: (451)
234 <220> FEATURE:
235 <221> NAME/KEY: unsure
236 <222> LOCATION: (456)
238 <220> FEATURE:
239 <221> NAME/KEY: unsure
240 <222> LOCATION: (478)
242 <220> FEATURE:
243 <221> NAME/KEY: unsure
244 <222> LOCATION: (480)
246 <220> FEATURE:
247 <221> NAME/KEY: unsure
248 <222> LOCATION: (490)
250 <220> FEATURE:
251 <221> NAME/KEY: unsure
252 <222> LOCATION: (510)
254 <220> FEATURE:
255 <221> NAME/KEY: unsure
256 <222> LOCATION: (542)
258 <220> FEATURE:
259 <221> NAME/KEY: unsure
260 <222> LOCATION: (549)
262 <220> FEATURE:

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Input Set : A:\BB1294 USDIV Seq.txt

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263 <221> NAME/KEY: unsure
264 <222> LOCATION: (552)
266 <220> FEATURE:
267 <221> NAME/KEY: unsure
268 <222> LOCATION: (554)
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272 <222> LOCATION: (572)
274 <220> FEATURE:
275 <221> NAME/KEY: unsure
276 <222> LOCATION: (578)
278 <220> FEATURE:
279 <221> NAME/KEY: unsure
280 <222> LOCATION: (583)
282 <220> FEATURE:
283 <221> NAME/KEY: unsure
284 <222> LOCATION: (588)
286 <220> FEATURE:
287 <221> NAME/KEY: unsure
288 <222> LOCATION: (595)
290 <220> FEATURE:
291 <221> NAME/KEY: unsure
292 <222> LOCATION: (601)
294 <400> SEQUENCE: 5
295 aaccgcgat catcggtat acctaccagc tcgctgttct tgctgaagcc ctggagctat 60
296 atagcttcga tctgcgcagc acaggttgct tgcgcactag tgattagtga agaagatggc 120
297 ggcgcgtgac caccgagagc tgagcggcga cgaggactcc gtggtggcgg ccggagacct 180
298 ccgcgcggg ccgtggacgg tggaggagga catgctcctc gtcaactacg tcgccgcgca 240
299 cggcgagggc cgctggaacg cgctggcacg atgcgcaggg ctccggcgga cggggaagag 300
300 ctgccgcctg cgggtggtca actacctgcg gccggacctg cggcggggca acatcacggc 360
301 gcaagagcaa ctgctcatcc tggagctgca ctccgcgtgg ggcaaccgct ggtcaagatc 420
W--> 302 gcgcagcacc tccaagggca acgacaacga natcanaact actggcgcac cggttcanan 480
W--> 303 caccagcan ctcaatgcaa ctcaaagcan cgctcaagga ctcagcgcta atctggatgc 540
W--> 304 gngctccna angnaccgtc gacatccggg angggctnct ttngagcnca cccaacaaac 600
W--> 305 n 601
307 <210> SEQ ID NO: 6
308 <211> LENGTH: 120
309 <212> TYPE: PRT
310 <213> ORGANISM: Zea mays
312 <220> FEATURE:
313 <221> NAME/KEY: UNSURE
314 <222> LOCATION: (101)
316 <220> FEATURE:
317 <221> NAME/KEY: UNSURE
318 <222> LOCATION: (113)..(114)
320 <400> SEQUENCE: 6
321 Met Ala Ala Arg Asp His Arg Glu Leu Ser Gly Asp Glu Asp Ser Val
322 1 5 10 15
324 Val Ala Ala Gly Asp Leu Arg Arg Gly Pro Trp Thr Val Glu Glu Asp

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

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Input Set : A:\BB1294 USDIV Seq.txt

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:16 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:100 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:101 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:101 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:106 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:106 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:107 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:108 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:109 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:110 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:111 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:112 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:112 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:146 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:152 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:152 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:168 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:302 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:303 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:304 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:305 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:339 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:339 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:342 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:342 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:376 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:377 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:378 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:378 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:379 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:402 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8

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L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:638 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:659 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:689 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:825 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:828 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:828 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:829 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:830 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:21
L:830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:859 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:868 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:868 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:941 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:941 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:944 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:944 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:945 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:945 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:946 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:947 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23
L:947 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1000 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24
L:1000 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1012 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24
L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1015 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24
L:1015 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1018 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24
L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1021 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24
L:1021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1192 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1192 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1193 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1194 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1196 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1197 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
L:1197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27

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L:1198 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
 L:1198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
 L:1199 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27
 L:1199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
 L:1222 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
 L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28